

Application No.: 10/521,351

Docket No.: H6808.0071/P071

**IN THE CLAIMS**

1-4. (Canceled)

5. (Previously presented) A method for processing information on nucleotide sequence, comprising steps of:

(a) receiving positional information representing a position in a nucleotide sequence in accordance with a request for an object and/or service;

(b) obtaining, from among a plurality of pieces of polymorphism pattern, a polymorphism pattern associated with the positional information received in step (a), wherein the obtained polymorphism pattern is information on nucleotide sequence which differs among individual organisms and shows a pattern of nucleotide or nucleotide sequence in a polymorphism;

(c) transmitting the polymorphism pattern obtained in step (b); and

(d) receiving semantic information corresponding to the polymorphism pattern transmitted in step (c) and/or information associated with the semantic information in association with positional information, wherein the semantic information refers to information on phenotypes caused by one or more differences in polymorphism patterns; and

wherein the method further comprises step (e) of making a determination as to whether the positional information received in step (d) matches positional information related to the polymorphism pattern transmitted in step (c); and

wherein step (e) comprises alerting a party that received the polymorphism pattern transmitted in step (c), and wherein the step of alerting is performed in response to the determination made in step (e).

6. (Previously presented) A method for processing information on nucleotide sequence, comprising steps of:

(a) receiving positional information representing a position in a nucleotide sequence in accordance with a request for an object and/or service;

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(b) obtaining, from among a plurality of pieces of polymorphism pattern, a polymorphism pattern associated with the positional information received in step (a), wherein the obtained polymorphism pattern is information on nucleotide sequence which differs among individual organisms and shows a pattern of nucleotide or nucleotide sequence in a polymorphism;

(c) transmitting the polymorphism pattern obtained in step (b); and

(d) receiving semantic information corresponding to the polymorphism pattern transmitted in step (c) and/or information associated with the semantic information in association with positional information, wherein the semantic information refers to information on phenotypes caused by one or more differences in polymorphism patterns; and

wherein the method further comprises step (e) of making a determination as to whether the positional information received in step (d) matches positional information related to the polymorphism pattern transmitted in step (c); and

wherein step (e) comprises disclosing information concerning a party that received the polymorphism pattern transmitted in step (c) to a third party, and wherein the third party is an organization for ensuring compliance with rules concerning transmission/reception of positional information or polymorphism pattern through a communication network, and wherein the step of disclosing is performed in response to the determination made in step (e).

7-12. (Canceled)

13. (Previously presented) A method for processing information on nucleotide sequence, comprising steps of: (a) receiving positional information representing a position in a nucleotide sequence in accordance with a request for an object and/or service; (b) obtaining, from among a plurality of pieces of polymorphism pattern, a polymorphism pattern associated with the positional information received in step (a), wherein the obtained polymorphism pattern is information on nucleotide sequence which differs among individual organisms and shows a pattern of nucleotide or nucleotide sequence in a polymorphism; (c) transmitting the polymorphism pattern obtained in step (b); and (d) receiving information corresponding to the

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polymorphism pattern transmitted in step (c) and/or information associated with the corresponding information in association with positional information; and

wherein the method further comprises step (e) of making a determination as to whether the positional information received in step (d) matches positional information related to the polymorphism pattern transmitted in step (c); and

wherein step (e) comprises alerting a party that received the polymorphism pattern transmitted in step (c), and wherein the step of alerting is performed in response to the determination made in step (e).

14. (Previously presented) The method of claim 13, wherein the corresponding information includes information on responsiveness to medicaments, side-effects caused by medicaments, risk of diseases and disorders, diatheses and properties, or interaction among proteins.

15. (Previously presented) The method of claim 13, wherein step (e) includes determining that there is no match between the positional information received in step (d) and the positional information related to the polymorphism pattern transmitted in step (c).

16. (Previously presented) A method for processing information on nucleotide sequence, comprising steps of: (a) receiving positional information representing a position in a nucleotide sequence in accordance with a request for an object and/or service; (b) obtaining, from among a plurality of pieces of polymorphism pattern, a polymorphism pattern associated with the positional information received in step (a), wherein the obtained polymorphism pattern is information on nucleotide sequence which differs among individual organisms and shows a pattern of nucleotide or nucleotide sequence in a polymorphism; (c) transmitting the polymorphism pattern obtained in step (b); and (d) receiving information corresponding to the polymorphism pattern transmitted in step (c) and/or information associated with the corresponding information in association with positional information; and

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wherein the method further comprises step (e) of making a determination as to whether the positional information received in step (d) matches positional information related to the polymorphism pattern transmitted in step (c); and

wherein step (e) comprises disclosing information concerning a party that received the polymorphism pattern transmitted in step (c) to a third party, and wherein the third party is an organization for ensuring compliance with rules concerning transmission/reception of positional information or polymorphism pattern through a communication network, and wherein the step of disclosing is performed in response to the determination made in step (e).

17. (Previously presented) The method of claim 16, wherein the corresponding information includes information on responsiveness to medicaments, side-effects caused by medicaments, risk of diseases and disorders, diatheses and properties, or interaction among proteins.

18. (Previously presented) The method of claim 16, wherein step (e) includes determining that there is no match between the positional information received in step (d) and the positional information related to the polymorphism pattern transmitted in step (c).

19. (Previously presented) The method of claim 5, wherein the information on phenotypes caused by one or more differences in polymorphism patterns includes information on responsiveness to medicaments.

20. (Previously presented) The method of claim 5, wherein the information on phenotypes caused by one or more differences in polymorphism patterns includes information on side-effects caused by medicaments.

21. (Previously presented) The method of claim 5, wherein the information on phenotypes caused by one or more differences in polymorphism patterns includes information on risk of diseases and disorders.

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22. (Previously presented) The method of claim 5, wherein the information on phenotypes caused by one or more differences in polymorphism patterns includes information on diatheses and properties.

23. (Previously presented) The method of claim 5, wherein the information on phenotypes caused by one or more differences in polymorphism patterns includes information on interaction among proteins.

24. (Previously presented) The method of claim 6, wherein the information on phenotypes caused by one or more differences in polymorphism patterns includes information on responsiveness to medicaments.

25. (Previously presented) The method of claim 6, wherein the information on phenotypes caused by one or more differences in polymorphism patterns includes information on side-effects caused by medicaments.

26. (Previously presented) The method of claim 6, wherein the information on phenotypes caused by one or more differences in polymorphism patterns includes information on risk of diseases and disorders.

27. (Previously presented) The method of claim 6, wherein the information on phenotypes caused by one or more differences in polymorphism patterns includes information on diatheses and properties.

28. (Previously presented) The method of claim 6, wherein the information on phenotypes caused by one or more differences in polymorphism patterns includes information on interaction among proteins.

29. (New) The method of claim 5, wherein step (e) further comprises transmitting a warning that is made based on an evaluation that the probability of unauthorized use and

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acquisition is high, a notification that all the transmitted polymorphism patterns were not used, or an announcement regarding notification to a third party that all the transmitted polymorphism patterns were not used.

30. (New) The method of claim 6, wherein step (e) further comprises transmitting a warning that is made based on an evaluation that the probability of unauthorized use and acquisition is high, a notification that all the transmitted polymorphism patterns were not used, or an announcement regarding notification to a third party that all the transmitted polymorphism patterns were not used.

31. (New) The method of claim 13, wherein step (e) further comprises transmitting a warning that is made based on an evaluation that the probability of unauthorized use and acquisition is high, a notification that all the transmitted polymorphism patterns were not used, or an announcement regarding notification to a third party that all the transmitted polymorphism patterns were not used.